

DNA sequences give evidence for evolutionary relationships

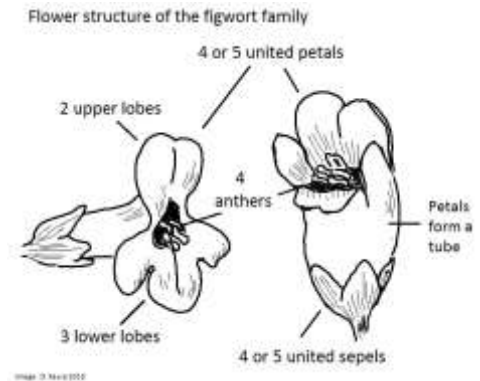
A new method is beginning to provide a lot of new evidence about how groups of living things are related. This method takes a few genes and compares the base sequence of these genes in several related species.

Imagine a single gene just a few hundred nucleotide bases long.
Here is a short extract of 30 bases in 3 species.

Species A: CATCATCATCATCATCATCATCATCATCAT

Species B: CATCAT**TACTACTACTAC**CATCATCATCAT

Species C: CATCAT**TACTACTACTAC**CATCAT**TAT**CAT



In the DNA of these species there looks to have been two mutations.

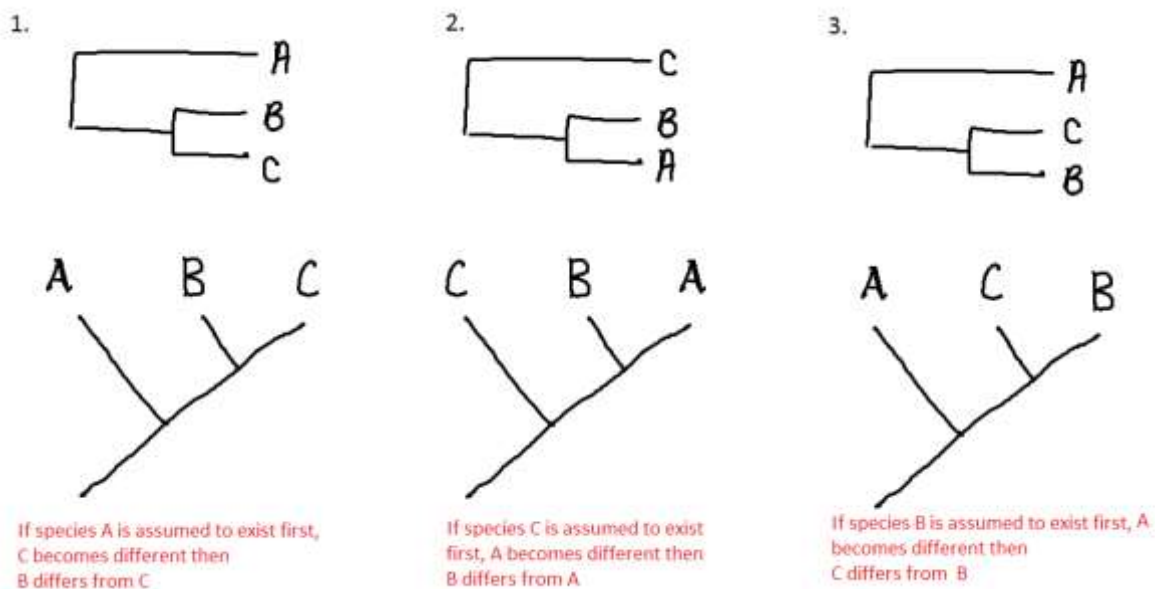
- In red, CATCATCATCAT has become inverted and now reads TACTACTACTAC.
- In blue a base C has been substituted by a base T

Of course both of these mutations could have happened in reverse. TAC could have become CAT and T could have become C. Is it possible to identify which base sequence came first?

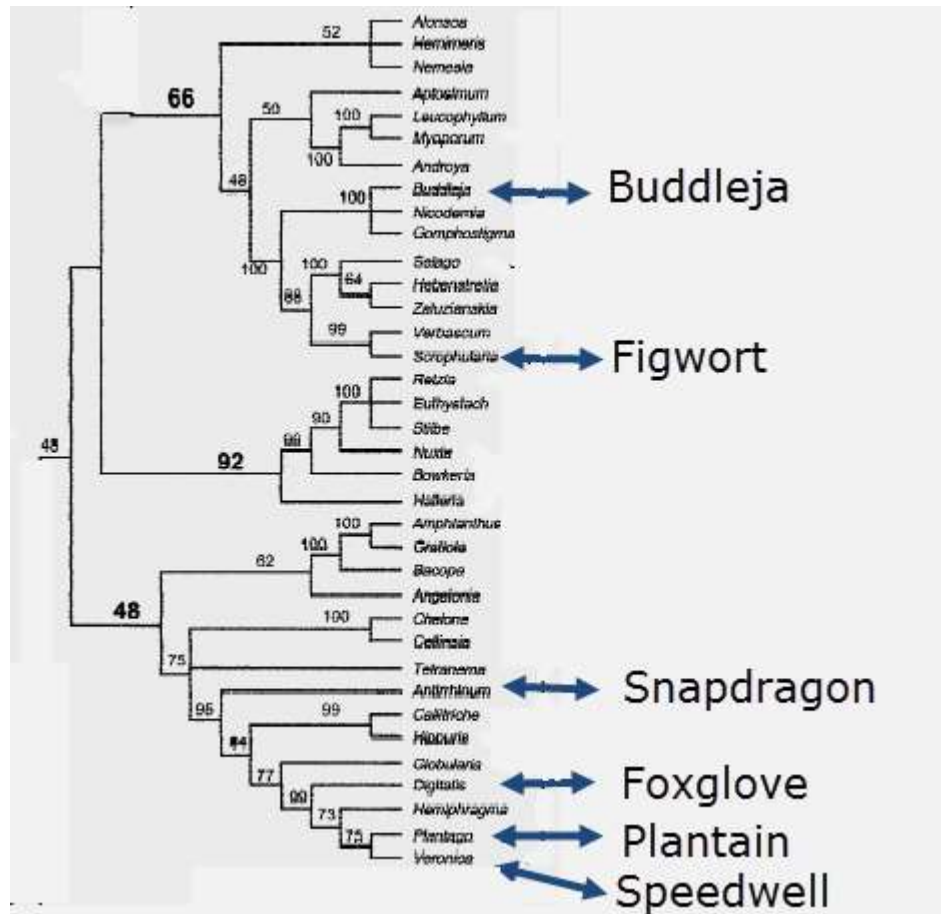
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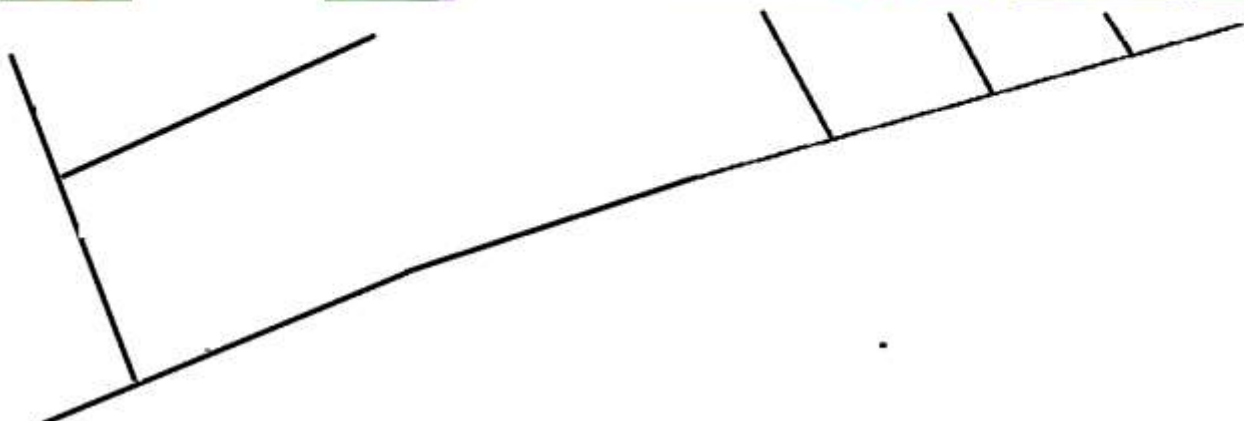
There are (at least) 3 possibilities. Follow the sequences of mutations in the 3 examples and identify which of these is the simplest sequence of mutations. The simplest one is the best explanation.



In a recent study (Olmstead et al 2001) three genes totalling 4200 bases were compared across 65 species. The results were analysed by a computer program to try to give the simplest explanation of the differences found. This extract of the cladogram is adapted from the data.



This is a simplified cladogram. Compare this to the first cladogram drawn from the flower features.



Questions

1. Which of the flowers are found in unexpected places on the DNA cladogram?

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2. What does this mean about the physical features of the flowers?
Are they homologous structures inherited from a common ancestor?

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3. "This is the beginning of an era of great advancement in classification", said Richard Olmstead. What was he referring to?

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